



DPPIV-5001-C1 PatentIn Replacement Sequence.ST25
REPLACEMENT SEQUENCE LISTING

<110> Takeda San Diego, Inc.
<120> CRYSTALLIZATION OF DIPEPTIDYL PEPTIDASE IV (DPPIV)
<130> DPPIV-5001-C1
<140> 10/659,055
<141> 2003-09-09
<150> US 60/409,206
<151> 2002-09-09
<160> 3
<170> PatentIn version 3.3
<210> 1
<211> 766
<212> PRT
<213> Homo sapiens

<220>
<221> Amino acid sequence for full-length human wild type DPPIV
<222> (1)..(766)

<300>
<308> Genbank/NP_001926
<309> 2002-02-19
<313> (1)..(766)

<400> 1
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Leu Val Thr Ile Ile Thr Val Pro Val Val Leu Leu Asn Lys Gly Thr
20 25 30
Asp Asp Ala Thr Ala Asp Ser Arg Lys Thr Tyr Thr Leu Thr Asp Tyr
35 40 45
Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr Ser Leu Arg Trp Ile Ser
50 55 60
Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn Asn Ile Leu Val Phe Asn
65 70 75 80
Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu Glu Asn Ser Thr Phe Asp
85 90 95
Glu Phe Gly His Ser Ile Asn Asp Tyr Ser Ile Ser Pro Asp Gly Gln
100 105 110

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Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys Gln Trp Arg His Ser Tyr
 115 120 125
 Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn Lys Arg Gln Leu Ile Thr
 130 135 140
 Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp Val Thr Trp Ser Pro Val
 145 150 155 160
 Gly His Lys Leu Ala Tyr Val Trp Asn Asn Asp Ile Tyr Val Lys Ile
 165 170 175
 Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr Trp Thr Gly Lys Glu Asp
 180 185 190
 Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val Tyr Glu Glu Glu Val Phe
 195 200 205
 Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala
 210 215 220
 Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro Leu Ile Glu Tyr Ser Phe
 225 230 235 240
 Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys Thr Val Arg Val Pro Tyr
 245 250 255
 Pro Lys Ala Gly Ala Val Asn Pro Thr Val Lys Phe Phe Val Val Asn
 260 265 270
 Thr Asp Ser Leu Ser Ser Val Thr Asn Ala Thr Ser Ile Gln Ile Thr
 275 280 285
 Ala Pro Ala Ser Met Leu Ile Gly Asp His Tyr Leu Cys Asp Val Thr
 290 295 300
 Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln Trp Leu Arg Arg Ile Gln
 305 310 315 320
 Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr Asp Glu Ser Ser Gly Arg
 325 330 335
 Trp Asn Cys Leu Val Ala Arg Gln His Ile Glu Met Ser Thr Thr Gly
 340 345 350
 Trp Val Gly Arg Phe Arg Pro Ser Glu Pro His Phe Thr Leu Asp Gly
 355 360 365

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Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu Glu Gly Tyr Arg His Ile
 370 375 380
 Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys Thr Phe Ile Thr Lys Gly
 385 390 395 400
 Thr Trp Glu Val Ile Gly Ile Glu Ala Leu Thr Ser Asp Tyr Leu Tyr
 405 410 415
 Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro Gly Gly Arg Asn Leu Tyr
 420 425 430
 Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val Thr Cys Leu Ser Cys Glu
 435 440 445
 Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser Val Ser Phe Ser Lys Glu
 450 455 460
 Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly Pro Gly Leu Pro Leu Tyr
 465 470 475 480
 Thr Leu His Ser Ser Val Asn Asp Lys Gly Leu Arg Val Leu Glu Asp
 485 490 495
 Asn Ser Ala Leu Asp Lys Met Leu Gln Asn Val Gln Met Pro Ser Lys
 500 505 510
 Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr Lys Phe Trp Tyr Gln Met
 515 520 525
 Ile Leu Pro Pro His Phe Asp Lys Ser Lys Lys Tyr Pro Leu Leu Leu
 530 535 540
 Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys Ala Asp Thr Val Phe Arg
 545 550 555 560
 Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala
 565 570 575
 Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His
 580 585 590
 Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu
 595 600 605
 Ala Ala Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asn Lys Arg Ile
 610 615 620

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Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu
625 630 635 640

Gly Ser Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val
645 650 655

Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr Thr Glu Arg Tyr Met Gly
660 665 670

Leu Pro Thr Pro Glu Asp Asn Leu Asp His Tyr Arg Asn Ser Thr Val
675 680 685

Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His
690 695 700

Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Ile Ser
705 710 715 720

Lys Ala Leu Val Asp Val Gly Val Asp Phe Gln Ala Met Trp Tyr Thr
725 730 735

Asp Glu Asp His Gly Ile Ala Ser Ser Thr Ala His Gln His Ile Tyr
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Thr His Met Ser His Phe Ile Lys Gln Cys Phe Ser Leu Pro
755 760 765

<210> 2
<211> 2184
<212> DNA
<213> Homo sapiens

<220>
<221> Human cDNA sequence encoding residues 39-766 of DPPIV
<222> (1)..(2184)

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ttcaatgctg aatatggaaa cagctcagtt ttcttgagaga acagtacatt tgatgagttt 180
ggacattcta tcaatgatta ttcaatatct cctgatgggc agttttattct cttagaatac 240
aactacgtga agcaatggag gcattcctac acagcttcat atgacattta tgatttaaata 300
aaaaggcagc tgattacaga agagaggatt ccaacaaca cacagtgggt cacatgggtca 360
ccagtgggtc ataaattggc atatgtttgg aacaatgaca tttatgttaa aattgaacca 420

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aattttaccaa gttacagaat cacatggacg gggaaagaag atataatata taatggaata	480
actgactggg tttatgaaga ggaagtcttc agtgcctact ctgctctgtg gtgggtctcca	540
aacggcactt ttttagcata tgcccaattt aacgacacag aagtcccact tattgaatac	600
tccttctact ctgatgagtc actgcagtac ccaaagactg tacgggttcc atatccaaag	660
gcaggagctg tgaatccaac tgtaaagttc tttgttgtaa atacagactc tctcagctca	720
gtcaccaatg caacttccat acaaactact gtcctgctt ctatgttgat aggggatcac	780
tacttggtg atgtgacatg ggcaacacaa gaaagaattt ctttgcagtg gctcaggagg	840
attcagaact attcgggtcat ggatatttgt gactatgatg aatccagtgg aagatggaac	900
tgcttagtg cagggcaaca cattgaaatg agtactactg gctgggttg aagatttagg	960
ccttcagaac ctcatTTTTac ccttgatggt aatagcttct acaagatcat cagcaatgaa	1020
gaagggttaca gacacatttg ctattttccaa atagataaaa aagactgcac atttattaca	1080
aaaggcacct ggggaagtc cgggatagaa gctctaacca gtgattatct atactacatt	1140
agtaatgaat ataaaggaat gccaggagga aggaatcttt ataaaatcca acttattgac	1200
tatacaaaaag tgacatgcct cagttgtgag ctgaatccgg aaagggtgtca gtactattct	1260
gtgtcattca gtaaagaggc gaagtattat cagctgagat gttccgggtcc tgggtctgccc	1320
ctctatactc tacacagcag cgtgaatgat aaagggtgga gagtcctgga agacaattca	1380
gctttggata aaatgctgca gaatgtccag atgccctcca aaaaactgga cttcattatt	1440
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aaatatcctc tactattaga tgtgtatgca ggcccatgta gtcaaaaagc agacactgtc	1560
ttcagactga actgggccac ttaccttgca agcacagaaa acattatagt agctagcttt	1620
gatggcagag gaagtgggta ccaaggagat aagatcatgc atgcaatcaa cagaagactg	1680
ggaacatttg aagttgaaga tcaaattgaa gcagccagac aattttcaaa aatgggattt	1740
gtggacaaca aacgaattgc aatttggggc tgggtcatatg gaggggtacgt aacctcaatg	1800
gtcctgggat cgggaagtgg cgtgttcaag tgtggaatag ccgtggcgcc tgtatccccg	1860
tgggagtact atgactcagt gtacacagaa cgttacatgg gtctcccaac tccagaagac	1920
aaccttgacc attacagaaa ttcaacagtc atgagcagag ctgaaaattt taaacaagtt	1980
gagtacctcc ttattcatgg aacagcagat gataacgttc actttcagca gtcagctcag	2040
atctccaaag ccctggtcga tgttgagtg gatttccagg caatgtggta tactgatgaa	2100
gaccatggaa tagctagcag cacagcacac caacatatat ataccacat gagccacttc	2160
ataaaacaat gtttctcttt acct	2184

<210> 3
<211> 740

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<212> PRT

<213> Homo sapiens

<220>

<221> N-terminal tag including a partial gp67 signal sequence and 6x-histidine

<222> (1)..(12)

<220>

<221> Amino acid sequence for residues 39-766 of DPPIV with an N-terminal tag

<222> (13)..(740)

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Tyr Thr Leu Thr Asp Tyr Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr
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Ser Leu Arg Trp Ile Ser Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn
35 40 45

Asn Ile Leu Val Phe Asn Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu
50 55 60

Glu Asn Ser Thr Phe Asp Glu Phe Gly His Ser Ile Asn Asp Tyr Ser
65 70 75 80

Ile Ser Pro Asp Gly Gln Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys
85 90 95

Gln Trp Arg His Ser Tyr Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn
100 105 110

Lys Arg Gln Leu Ile Thr Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp
115 120 125

Val Thr Trp Ser Pro Val Gly His Lys Leu Ala Tyr Val Trp Asn Asn
130 135 140

Asp Ile Tyr Val Lys Ile Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr
145 150 155 160

Trp Thr Gly Lys Glu Asp Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val
165 170 175

Tyr Glu Glu Glu Val Phe Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro
180 185 190

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Asn Gly Thr Phe Leu Ala Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro
195 200 205

Leu Ile Glu Tyr Ser Phe Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys
210 215 220

Thr Val Arg Val Pro Tyr Pro Lys Ala Gly Ala Val Asn Pro Thr Val
225 230 235 240

Lys Phe Phe Val Val Asn Thr Asp Ser Leu Ser Ser Val Thr Asn Ala
245 250 255

Thr Ser Ile Gln Ile Thr Ala Pro Ala Ser Met Leu Ile Gly Asp His
260 265 270

Tyr Leu Cys Asp Val Thr Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln
275 280 285

Trp Leu Arg Arg Ile Gln Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr
290 295 300

Asp Glu Ser Ser Gly Arg Trp Asn Cys Leu Val Ala Arg Gln His Ile
305 310 315 320

Glu Met Ser Thr Thr Gly Trp Val Gly Arg Phe Arg Pro Ser Glu Pro
325 330 335

His Phe Thr Leu Asp Gly Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu
340 345 350

Glu Gly Tyr Arg His Ile Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys
355 360 365

Thr Phe Ile Thr Lys Gly Thr Trp Glu Val Ile Gly Ile Glu Ala Leu
370 375 380

Thr Ser Asp Tyr Leu Tyr Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro
385 390 395 400

Gly Gly Arg Asn Leu Tyr Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val
405 410 415

Thr Cys Leu Ser Cys Glu Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser
420 425 430

Val Ser Phe Ser Lys Glu Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly
435 440 445

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Pro Gly Leu Pro Leu Tyr Thr Leu His Ser Ser Val Asn Asp Lys Gly
450 455 460

Leu Arg Val Leu Glu Asp Asn Ser Ala Leu Asp Lys Met Leu Gln Asn
465 470 475 480

Val Gln Met Pro Ser Lys Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr
485 490 495

Lys Phe Trp Tyr Gln Met Ile Leu Pro Pro His Phe Asp Lys Ser Lys
500 505 510

Lys Tyr Pro Leu Leu Leu Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys
515 520 525

Ala Asp Thr Val Phe Arg Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr
530 535 540

Glu Asn Ile Ile Val Ala Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln
545 550 555 560

Gly Asp Lys Ile Met His Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu
565 570 575

Val Glu Asp Gln Ile Glu Ala Ala Arg Gln Phe Ser Lys Met Gly Phe
580 585 590

Val Asp Asn Lys Arg Ile Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr
595 600 605

Val Thr Ser Met Val Leu Gly Ser Gly Ser Gly Val Phe Lys Cys Gly
610 615 620

Ile Ala Val Ala Pro Val Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr
625 630 635 640

Thr Glu Arg Tyr Met Gly Leu Pro Thr Pro Glu Asp Asn Leu Asp His
645 650 655

Tyr Arg Asn Ser Thr Val Met Ser Arg Ala Glu Asn Phe Lys Gln Val
660 665 670

Glu Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn Val His Phe Gln
675 680 685

Gln Ser Ala Gln Ile Ser Lys Ala Leu Val Asp Val Gly Val Asp Phe
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690 DPPIV-5001-C1 PatentIn Replacement Sequence.ST25
695 700

Gln Ala Met Trp Tyr Thr Asp Glu Asp His Gly Ile Ala Ser Ser Thr
705 710 715 720

Ala His Gln His Ile Tyr Thr His Met Ser His Phe Ile Lys Gln Cys
725 730 735

Phe Ser Leu Pro
740